

APPROVED	O.G. FIG.
	CLASS/SUBCLASS
BY	DRAFTSMAN

WO 99/18976

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FIG. 1A
HUMAN SEGMENT E: (SEQ ID NOS:1-2)

ATG AGA TGG CGA CGC GCC CCG CGC CGC TCC GGG CGT CCC GGC CCC CGG Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg 1 5 10 15	48
GCC CAG CGC CCC GGC TCC GCC GCC CGC TCG TCG CCG CCG CTG CCG CTG Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu 20 25 30	96
CTG CCA CTA CTG CTG CTG CTG GGG ACC GCG GCC CTG GCG CCG GGG GCG Leu Pro Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala 35 40 45	144
GCG GCC GGC AAC GAG GCG GCT CCC GCG GGG GCC TCG GTG TGC TAC TCG Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser 50 55 60	192
TCC CCG CCC AGC GTG GGA TCG GTG CAG GAG CTA GCT CAG CGC GCC GCG Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala 65 70 75 80	240
GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CGG CGG CAG CAG GGG GCA Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala 85 90 95	288
CTC GAC AGG AAG GCG GCG GCG GCG GCG GGC GAG GCA GGG GCG TGG GGC Leu Asp Arg Lys Ala Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly 100 105 110	336
GGC GAT CGC GAG CCG CCA GCC GCG GGC CCA CGG GCG CTG GGG CCG CCC Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro 115 120 125	384
GCC GAG GAG CCG CTG CTC GCC GCC AAC GGG ACC GTG CCC TCT TGG CCC Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro 130 135 140	432
ACC GCC CCG GTG CCC AGC GCC GGC GAG CCC GGG GAG GAG GCG CCC TAT Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr 145 150 155 160	480
CTG GTG AAG GTG CAC CAG GTG TGG GCG GTG AAA GCC GGG GGC TTG AAG Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys 165 170 175	528
AAG GAC TCG CTG CTC ACC GTG CGC CTG GGG ACC TGG GGC CAC CCC GCC Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala 180 185 190	576

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FIG. 1B

TTC CCC TCC TGC GGG AGG CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC	624
Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe	
195 200 205	
ATG GAG CCC GAC GCC AAC AGC ACC AGC CGC GCG CCG GCC GCC TTC CGA	672
Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg	
210 215 220	
GCC TCT TTC CCC CCT CTG GAG ACG GGC CGG AAC CTC AAG AAG GAG GTC	720
Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val	
225 230 235 240	
AGC CGG GTG CTG TGC AAG CGG TGC G	745
Ser Arg Val Leu Cys Lys Arg Cys	
245	

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FIG. 2
SEGMENT E: (SEQ ID NOS:3-4)

CC CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG	47
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser	15
1 5 10	
CTG CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC	95
Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser	30
20 25	
TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC	143
Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro	45
35 40	
GAG GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC	191
Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro	60
50 55	
CCC TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT	239
Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala	75
65 70	
GTG CAA CGG TGC G	252
Val Gln Arg Cys	
80	

FIG. 3
SEGMENT B: (SEQ ID NOS:5-8)

Leu Pro Pro Arg Leu Lys Glu His Lys Ser Gln Glu Ser Val Ala Gly	48
CCT TGC CTC CCC GCT TGA AAG AGA TGA AGA GTC AGG AGT CTG TGG CAG	
CCT TGC CTC CCC GAT TGA AAG AGA TGA AAA GCC AGG AAT CGG CTG CAG	
Q	
Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu	96
GTT CCA AAC TAG TGC TTC GGT GCG AGA CCA GTT CTG AAT ACT CCT CTC	
GTT CCA AAC TAG TCC TTC GGT GTG AAA CCA GTT CTG AAT ACT CCT CTC	
Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys	144
TCA AGT TCA AGT GGT TCA AGA ATG GGA GTG AAT TAA GCC GAA AGA ACA	
TCA GAT TCA AGT GGT TCA AGA ATG GGA ATG AAT TGA ATC GAA AAA ACA	
R N N	
Pro Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly	178
AAC CAC AAA ACA TCA AGA TAC AGA AAA GGC CGG G	
AAC CAC AAA ATA TCA AGA TAC AAA AAA AGC CAG G	
K	

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FIG 4
SEGMENT A: (SEQ ID NOS:9-12)

Lys	Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly		46
G AAG	TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	CTG	GCT	GAT	TCT	GGA		
G AAG	TCA	GAA	CTT	CGC	ATT	AAC	AAA	GCA	TCA	CTG	GCT	GAT	TCT	GGA		
N																
Glu	Tyr	Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	94
GAA	TAT	ATG	TGC	AAA	GTG	ATC	AGC	AAA	CTA	GGA	AAT	GAC	AGT	GCC	TCT	
GAG	TAT	ATG	TGC	AAA	GTG	ATC	AGC	AAA	TTA	GGA	AAT	GAC	AGT	GCC	TCT	
Ala	Asn	Ile	Thr	Ile	Val	Glu	Ser	Asn	Ala							122
GCC	AAC	ATC	ACC	ATT	GTG	GAG	TCA	AAC	G							
GCC	AAT	ATC	ACC	ATC	GTG	GAA	TCA	AAC	G							

FIG.5
SEGMENT A': (SEQ ID NOS:13-14)

TCTAAACTA CAGAGACTGT ATTTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC	60
CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG	110
Lys Ser Glu Leu Arg Ile Ser Lys Ala	
1 5	
TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA	158
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu	
10 15 20 25	
GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT	206
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly	
30 35 40	
AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC	254
Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile	
45 50 55	
AAG GTA TGT GGT CAC ACT TGAATCACGC AGGTGTGTGA AATCTCATTG	302
Lys Val Cys Gly His Thr	
60	
TGAACAAATA AAAATCATGA AAGGAAACT CTATGTTTGA AATATCTTAT GGGTCCTCCT	362
GTAAGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATTT	417

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FIG. 6
SEGMENT G: (SEQ ID NOS:15-18)

Glu	Ile	Thr	Thr	Gly	Met	Pro	Ala	Ser	Thr	Glu	Thr	Ala	Tyr	Val	Ser	
AG	ATC	ACC	ACT	GGC	ATG	CCA	GCC	TCA	ACT	GAG	ACA	GCG	TAT	GTG	TCT	47
AG	ATC	ATC	ACT	GGT	ATG	CCA	GCC	TCA	ACT	GAA	GGA	GCA	TAT	GTG	TCT	
			I							G						

Ser	Glu	Ser	Pro	Ile	Arg	Ile	Ser	Val	Ser	Thr	Glu	Gly	Thr	Asn	Thr	
TCA	GAG	TCT	CCC	ATT	AGA	ATA	TCA	GTA	TCA	ACA	GAA	GGA	ACA	AAT	ACT	95
TCA	GAG	TCT	CCC	ATT	AGA	ATA	TCA	GTA	TCC	ACA	GAA	GGA	GCA	AAT	ACT	
													A			

Ser	Ser	Ser														
TCT	TCA	T														102
TCT	TCA	T														

FIG. 7
SEGMENT C: (SEQ ID NOS:19-22)

Thr	Ser	Thr	Ser	Thr	Ala	Gly	Thr	Ser	His	Leu	Val	Lys	Cys	Ala		
CC	ACA	TCC	ACA	TCT	ACA	GCT	GGG	ACA	AGC	CAT	CTT	GTC	AAG	TGT	GCA	47
CT	ACA	TCT	ACA	TCC	ACC	ACT	GGG	ACA	AGC	CAT	CTT	GTA	AAA	TGT	GCG	
						T										

Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	Gly	Gly	Glu	Cys	Phe	Met	Val	
GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	GGA	GGC	GAG	TGC	TTC	ATG	GTG	95
GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	GGA	GGG	GAG	TGC	TTC	ATG	GTG	

Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	Leu	Cys						
AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	TTG	TGC						128
AAA	GAC	CTT	TCA	AAC	CCC	TCG	AGA	TAC	TTG	TGC						

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FIG. 8
SEGMENT C/D: (SEQ ID NOS:23-26)

Lys	Cys	Gln	Pro	Gly	Phe	Thr	Gly	Ala	Arg	Cys	Thr	Glu	Asn	Val	Pro	
AAG	TGC	CAA	CCT	GGA	TTC	ACT	GGA	GCG	AGA	TGT	ACT	GAG	AAT	GTG	CCC	48
AAG	TGC	CAA	CCT	GGA	TTC	ACT	GGA	GCA	AGA	TGT	ACT	GAG	AAT	GTG	CCC	
Met	Lys	Val	Gln	Thr	Gln	Glu										
ATG	AAA	GTC	CAA	ACC	CAA	GAA										69
ATG	AAA	GTC	CAA	AAC	CAA	GAA										
				N												

FIG. 9
SEGMENT C/D': (SEQ ID NOS:27-29)

Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Met	
AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	GTA	ATG	48
AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	GTA	ATG	
Ala	Ser	Phe	Tyr													
GCC	AGC	TTC	TAC													60
GCC	AGC	TTC	TAC													

FIG. 10
SEGMENT D: (SEQ ID NOS:30-32)

Ser	Thr	Ser	Thr	Pro	Phe	Leu	Ser	Leu	Pro	Glu	*					
AGT	ACG	TCC	ACT	CCC	TTT	CTG	TCT	CTG	CCT	GAA	TAG					36
AGT	ACG	TCC	ACT	CCC	TTT	CTG	TCT	CTG	CCT	GAA	TAG					

FIG. 11
SEGMENT D': (SEQ ID NOS:33-34)

27

FIG. 12A
SEGMENT H: (SEQ ID NOS:35-38)

48

96

144

192

240

288

336

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FIG. 12B

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Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly His Thr Glu	384
ACT GTC ACT CAG ACT CCC AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA	
ACT GTC ACC CAG ACT CCT AGC CAC AGC TGG AGC AAC GGA CAC ACT GAA	
Ser Ile Ile Ser Glu Ser His Ser Val Ile Val Met Ser Ser Val Glu	432
AGC ATC ATT TCG GAA AGC CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA	
AGC ATC CTT TCC GAA AGC CAC TCT GTA ATC GTG ATG TCA TCC GTA GAA	
L	
Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn	480
AAC AGT AGG CAC AGC AGC CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT	
AAC AGT AGG CAC AGC AGC CCA ACT GGG GGC CCA AGA GGA CGT CTT AAT	
Gly Leu Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala Arg	528
GGC TTG GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA	
GGC ACA GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA	
T	
Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg	569
GAA ACC CCT GAC TCC TAC CGA GAC TCT CCT CAT AGT GAA AG	
GAA ACC CCT GAT TCC TAC CGA GAC TCT CCT CAT AGT GAA AG	

FIG. 13

SEGMENT K: (SEQ ID NOS:39-40)

A CAT AAC CTT ATA GCT GAG CTA AGG AGA AAC AAG GCC CAC AGA TCC	46
His Asn Leu Ile Ala Glu Leu Arg Arg Asn Lys Ala His Arg Ser	
1 5 10 15	
AAA TGC ATG CAG ATC CAG CTT TCC GCA ACT CAT CTT AGA GCT TCT TCC	94
Lys Cys Met Gln Ile Gln Leu Ser Ala Thr His Leu Arg Ala Ser Ser	
20 25 30	
ATT CCC CAT TGG GCT TCA TTC TCT AAG ACC CCT TGG CCT TTA GGA AG	141
Ile Pro His Trp Ala Ser Phe Ser Lys Thr Pro Trp Pro Leu Gly Arg	
35 40 45	

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FIG. 14A
SEGMENT L: (SEQ ID NOS:41-44)

APPROVED	O.G. FIG.
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Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp
G TAT GTA TCA GCA ATG ACC ACC CCG GCT CGT ATG TCA CCT GTA GAT 46
G TAT GTG TCA GCC ATG ACC ACC CCG GCT CGT ATG TCA CCT GTA GAT

Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro
TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC CCT TCG GAA ATG TCC CCG 94
TTC CAC ACG CCA AGC TCC CCC AAA TCG CCC CCT TCG GAA ATG TCT CCA

Pro Val Ser Ser Thr Thr Val Ser Met Pro Ser Met Ala Val Ser Pro
CCC GTG TCC AGC ACG ACG GTC TCC ATG CCC TCC ATG GCG GTC AGT CCC 142
CCC GTG TCC AGC ATG ACG GTG TCC ATG CCT TCC ATG GCG GTC AGC CCC
M

Phe Val Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu
TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT GTG ACG CCA CCA CGG CTG 190
TTC ATG GAA GAA GAG AGA CCT CTA CTT CTC GTG ACA CCA CCA AGG CTG
N

Arg Glu Lys - Tyr Asp His His Ala Gln Gln Phe Asn Ser Phe His
CGG GAG AAG ... TAT GAC CAC CAC GCC CAG CAA TTC AAC TCG TTC CAC 238
CGG GAG AAG AAG TTT GAC CAT CAC CCT CAG CAG TTC AGC TCC TTC CAC
K F P

Cys Asn Pro Ala His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg
TGC AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC CCC AGC CCC TTG AGG 286
CAC AAC CCC GCG CAT GAG AGT AAC AGC CTC CCT GCT AGC CCC TTG AGG
N D A

Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala
ATA GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG GAG TAC GAA CCA GCT 334
ATA GTG GAG GAT GAG GAG TAT GAA ACG ACC CAA GAG TAC GAG CCA GCC

Gln Glu Pro Val Lys Lys Leu Thr Asn Ser Ser Arg Arg Ala Lys Arg
CAA GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC CCG CCG GCC AAA AGA 382
CAA GAG CCT GTT AAG AAA CTC GCC AA...T AGC CCG CCG GCC AAA AGA
A

FIG. 14B

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DRAFTSMAN		

Thr Lys Pro Asn Gly His Ile Ala His Arg Leu Glu Met Asp Asn Asn
ACC AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG GAA ATG GAC AAC AAC
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
ACC AAG CCC AAT GGC CAC ATT GCT AAC AGA TTG GAA GTG GAC AGC AAC
N V S

430

Thr Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu Arg
ACA GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA ACA GAG GAT GAA AGA
||| ||| |
ACA AGC TCC CAG AGC AGT AAC TCA GAG AGT GAA ACA GAA GAT GAA AGA
S S O

478

Val	Gly	Glu	Asp	Thr	Pro	Phe	Leu	Ala	Ile	Gln	Asn	Pro	Leu	Ala	Ala	
GTA	GGA	GAA	GAT	ACG	CCT	TTC	CTG	GCC	ATA	CAG	AAC	CCC	CTG	GCA	GCC	526
GTA	GGT	GAA	GAT	ACG	CCT	TTC	CTG	GGC	ATA	CAG	AAC	CCC	CTG	GCA	GCC	
								6								

Ser Leu Glu Ala Ala Pro Ala Phe Arg Leu Val Asp Ser Arg Thr Asn
AGT CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC GAC AGC AGG ACT AAC
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
AGT CTT GAG GCA ACA CCT GCC TTC CGC CTG GCT A

574

Pro Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu Gln Ala Arg Leu Ser
CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG CAG GCC AGG CTC TCC
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
CCA GCA GGC CGC TTC TCG ACA CAG GAA GAA ATC CAG GCC AGG CTG TCT
A R I I

622

[illegible]

CCC ATA GAT TCA CCT GTA AAA CTT TAT TTT ATA TAA TAA AGT ATT CCA 718
| | | | | | | | | | | | | | | | | |
CAC ATA GAT TCA CCT GTA AAA CTT TAT TTT ATA TAA TAA AGT ATT CCA

CCT TAA ATT AAA CAA
||| ||| ||| ||| |||
CCT TAA ATT AAA CAA

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FIG. 15
SEGMENT F: (SEQ ID NOS:45-48)

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AGTTTCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC      60
GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC      120
TGCGAGCGCG CCGGACCGAG GCACGCACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC      180
CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGNCGTGCG ACCGGGACGG AGCGCCCGCC      240
AGTCCCAGGT GGCCCGGACC GCACGTTGCG TCCCCGCGCT CCCGCGCGGC GACAGGAGAC      300
GCTCCCCCCC ACGCCGCGCG CGCCTCGGCC CGGTCGCTGG CCCGCCTCCA CTCCGGGGAC      360
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          CGCGAG CGCCTCAGCG CGGCCGCTCG CTCTC...CCC CTCGAGGGAC

AAACTTTTCC CGAAGCCGAT CCCAGCCCTC GGACCCAAAC TTGTCGCGCG TCGCCTTCGC      420
AAACTTTTCC CAAACCCGAT CCGAGCCCTT GGACCAA... ..C TCGCCTGCGC

                                Met Ser Glu Arg Arg
CGGGAGCCGT CCGCGCAGAG CGTGCACTTC TCGGGCGAG ATG TCG GAG CGC AGA      474
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CGAGAGCCGT CCGCGTAGAG CGCTC.CGTC TCCGGCGAG ATG TCC GAG CGC AAA
                                K

Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly
GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG      522
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GAA GGC AGA GGC AAA GGG AAG GGC AAG AAG AAG GAG CGA GGC TCC GGC
          R                                K                                E

Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala
AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA G      559
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AAG AAG CCG GAG TCC GCG GCG GGC AGC CAG AGC CCA G
          E      S

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FIG. 16A
(SEQ ID NOS:49-50)

G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA	49
Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu	
1 5 10 15	
TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC	97
Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala	
20 25 30	
AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG	145
Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly	
35 40 45	
ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG	193
Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val	
50 55 60	
AAT GGA GGC GAC TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA	241
Asn Gly Gly Asp Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg	
65 70 75 80	
TAC TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG	289
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu	
85 90 95	
AAT GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC	337
Asn Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr	
100 105 110	
CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT TGC ATC GCG CTG CTC GTG	385
Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val	
115 120 125	
GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC AAA ACC AAG AAA CAA CGG	433
Val Gly Ile Met Cys Val Val Val Tyr Cys Lys Thr Lys Lys Gln Arg	
130 135 140	
AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC CTT CGG TCT GAA AGA AAC	481
Lys Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn	
145 150 155 160	
ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC CAC CCC AAT CCG CCC CCC	529
Thr Met Met Asn Val Ala Asn Gly Pro His His Pro Asn Pro Pro Pro	
165 170 175	
GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA TCT AAA AAT GTC ATC TCT	577
Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser	
180 185 190	

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FIG. 16B

AGC Ser	GAG Glu	CAT His 195	ATT Ile	GTT Val	GAG Glu	AGA Arg	GAG Glu 200	GCG Ala	GAG Glu	AGC Ser	TCT Ser	TTT Phe 205	TCC Ser	ACC Thr	AGT Ser	625
CAC His	TAC Tyr 210	ACT Thr	TCG Ser	ACA Thr	GCT Ala	CAT His 215	CAT His	TCC Ser	ACT Thr	ACT Thr	GTC Val 220	ACT Thr	CAG Gln	ACT Thr	CCC Pro	673
AGT Ser 225	CAC His	AGC Ser	TGG Trp	AGC Ser	AAT Asn 230	GGA Gly	CAC His	ACT Thr	GAA Glu	AGC Ser 235	ATC Ile	ATT Ile	TCG Ser	GAA Glu	AGC Ser 240	721
CAC His	TCT Ser	GTC Val	ATC Ile	GTG Val 245	ATG Met	TCA Ser	TCC Ser	GTA Val	GAA Glu 250	AAC Asn	AGT Ser	AGG Arg	CAC His	AGC Ser 255	AGC Ser	769
CCG Pro	ACT Thr	GGG Gly 260	GGC Gly	CCG Pro	AGA Arg	GGA Gly	CGT Arg	CTC Leu 265	AAT Asn	GGC Gly	TTG Leu	GGA Gly	GGC Gly 270	CCT Pro	CGT Arg	817
GAA Glu 305	TGT Cys	AAC Asn 275	AGC Ser	TTC Phe	CTC Leu	AGG Arg	CAT His 280	GCC Ala	AGA Arg	GAA Glu	ACC Thr	CCT Pro 285	GAC Asp	TCC Ser	TAC Tyr	865
CGA Arg 290	GAC Asp	TCT Ser	CCT Pro	CAT His	AGT Ser	GAA Glu 295	AGA Arg	CAT His	AAC Asn	CTT Leu	ATA Ile 300	GCT Ala	GAG Glu	CTA Leu	AGG Arg	913
AGA Arg 305	AAC Asn	AAG Lys	GCC Ala	CAC His	AGA Arg 310	TCC Ser	AAA Lys	TGC Cys	ATG Met	CAG Gln 315	ATC Ile	CAG Gln	CTT Leu	TCC Ser	GCA Ala 320	961
ACT Thr	CAT His	CTT Leu	AGA Arg	GCT Ala 325	TCT Ser	TCC Ser	ATT Ile	CCC Pro	CAT His 330	TGG Trp	GCT Ala	TCA Ser	TTC Phe	TCT Ser 335	AAG Lys	1009
ACC Thr	CCT Pro	TGG Trp	CCT Pro 340	TTA Leu	GGA Gly	AGG Arg	TAT Tyr	GTA Val 345	TCA Ser	GCA Ala	ATG Met	ACC Thr	ACC Thr 350	CCG Pro	GCT Ala	1057
CGT Arg	ATG Met	TCA Ser 355	CCT Pro	GTA Val	GAT Asp	TTC Phe	CAC His 360	ACG Thr	CCA Pro	AGC Ser	TCC Ser	CCC Pro 365	AAG Lys	TCA Ser	CCC Pro	1105
CCT Pro 370	TCG Ser	GAA Glu	ATG Met	TCC Ser	CCG Pro	CCC Pro 375	GTG Val	TCC Ser	AGC Ser	ACG Thr	ACG Thr	GTC Val 380	TCC Ser	ATG Met	CCC Pro	1153

APPROVED BY	O.G. FIG.
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FIG. 16C

TCC ATG GCG GTC AGT CCC TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT 1201
 Ser Met Ala Val Ser Pro Phe Val Glu Glu Glu Arg Pro Leu Leu Leu
 385 390 395 400

GTG ACG CCA CCA CGG CTG CGG GAG AAG TAT GAC CAC CAC GCC CAG CAA 1249
 Val Thr Pro Pro Arg Leu Arg Glu Lys Tyr Asp His His Ala Gln Gln
 405 410 415

TTC AAC TCG TTC CAC TGC AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC 1297
 Phe Asn Ser Phe His Cys Asn Pro Ala His Glu Ser Asn Ser Leu Pro
 420 425 430

CCC AGC CCC TTG AGG ATA GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG 1345
 Pro Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln
 435 440 445

GAG TAC GAA CCA GCT CAA GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC 1393
 Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Thr Asn Ser Ser
 450 455 460

CGG CGG GCC AAA AGA ACC AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG 1441
 Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala His Arg Leu
 465 470 475 480

GAA ATG GAC AAC AAC ACA GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA 1489
 Glu Met Asp Asn Asn Thr Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu
 485 490 495

ACA GAG GAT GAA AGA GTA GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG 1537
 Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln
 500 505 510

AAC CCC CTG GCA GCC AGT CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC 1585
 Asn Pro Leu Ala Ala Ser Leu Glu Ala Ala Pro Ala Phe Arg Leu Val
 515 520 525

GAC AGC AGG ACT AAC CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG 1633
 Asp Ser Arg Thr Asn Pro Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu
 530 535 540

CAG GCC AGG CTC TCC GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC 1681
 Gln Ala Arg Leu Ser Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val
 545 550 555 560

TAAAACCGAA ATACACCCAT AGATTCACCT GTAAACTTT ATTTTATATA ATAAAGTATT 1741

CCACCTTAAA TTAACA AAA 1764

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FIG. 17A
(SEQ ID NOS:51-52)

CAT	CAA	GTG	TGG	GCG	GCG	AAA	GCC	GGG	GGC	TTG	AAG	AAG	GAC	TCG	CTG	48
His	Gln	Val	Trp	Ala	Ala	Lys	Ala	Gly	Gly	Leu	Lys	Lys	Asp	Ser	Leu	
1				5				10					15			
CTC	ACC	GTG	CGC	CTG	GGC	GCC	TGG	GGC	CAC	CCC	GCC	TTC	CCC	TCC	TGC	96
Leu	Thr	Val	Arg	Leu	Gly	Ala	Trp	Gly	His	Pro	Ala	Phe	Pro	Ser	Cys	
			20					25					30			
GGG	CGC	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	TTC	ATG	GAG	CCC	GAG	144
Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	Met	Glu	Pro	Glu	
			35				40					45				
GCC	AAC	AGC	AGC	GGC	GGG	CCC	GGC	CGC	CTT	CCG	AGC	CTC	CTT	CCC	CCC	192
Ala	Asn	Ser	Ser	Gly	Gly	Pro	Gly	Arg	Leu	Pro	Ser	Leu	Leu	Pro	Pro	
	50					55					60					
TCT	CGA	GAC	GGG	CCG	GAA	CCT	CAA	GAA	GGA	GGT	CAG	CCG	GGT	GCT	GTG	240
Ser	Arg	Asp	Gly	Pro	Glu	Pro	Gln	Glu	Gly	Gly	Gln	Pro	Gly	Ala	Val	
65				70				75						80		
CAA	CGG	TGC	GCC	TTG	CCT	CCC	CGC	TTG	AAA	GAG	ATG	AAG	AGT	CAG	GAG	288
Gln	Arg	Cys	Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	
				85				90						95		
TCT	GTG	GCA	GGT	TCC	AAA	CTA	GTG	CTT	CGG	TGC	GAG	ACC	AGT	TCT	GAA	336
Ser	Val	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu	
			100					105					110			
TAC	TCC	TCT	CTC	AAG	TTC	AAG	TGG	TTC	AAG	AAT	GGG	AGT	GAA	TTA	AGC	384
Tyr	Ser	Ser	Leu	Lys	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser	
			115				120					125				
CGA	AAG	AAC	AAA	CCA	GAA	AAC	ATC	AAG	ATA	CAG	AAA	AGG	CCG	GGG	AAG	432
Arg	Lys	Asn	Lys	Pro	Glu	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Gly	Lys	
	130					135					140					
TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	CTG	GCT	GAT	TCT	GGA	GAA	TAT	480
Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	
145				150				155						160		
ATG	TGC	AAA	GTG	ATC	AGC	AAA	CTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAC	528
Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn	
				165				170						175		

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FIG. 17B

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA	576
Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr	
180 185 190	
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	624
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
195 200 205	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	672
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
210 215 220	
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT	720
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	
225 230 235 240	
GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT	768
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr	
245 250 255	
GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC	816
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser	
260 265 270	
ACT CCC TTT CTG TCT CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG	870
Thr Pro Phe Leu Ser Leu Pro Glu	
275 280	
TTGCCGCATC TCCCCTCAGA TTCCNCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT	930
GACTGCCTCT GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC	990
CGTGACTAGT GGGCTCTGAG CTA CTCTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG	1050
ATCTTGAATT ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG	1110
GCCTTGAAAA GTCAAAAAA AAAAAAAAAA	1140

APPROVED	O.G. FIG.	CLASS	SUBCLASS
	BY		

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FIG. 18A
(SEQ ID NOS:53-54)

AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC	60
GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC	120
TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC	180
CCAGCGGGCG GCCAGCAGGA GCCACCCCGC GAGCGTGCGA CCGGACGGA GCGCCCGCCA	240
GTCCAGGTG GCGCGGACCG CACGTTGCGT CCGCGGCTC CCGCGGGCG ACAGGAGACG	300
CTCCCCCCCC CGCCGCGCGC GCCTCGGCCC GGTCGCTGGC CCGCCTCCAC TCCGGGGACA	360
AACTTTTCCC GAAGCCGATC CCAGCCCTCG GACCCAACT TGTCGCGCGT CGCCTTCGCC	420
GGGAGCCGTC CGCGCAGAGC GTGCACTTCT CGGGCGAG ATG TCG GAG CGC AGA	473
Met Ser Glu Arg Arg	5
GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG	521
Glu Gly Lys Gly Lys Gly Lys Gly Lys Lys Lys Asp Arg Gly Ser Gly	20
AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA GCC TTG CCT CCC	569
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala Leu Pro Pro	35
CGC TTG AAA GAG ATG AAG ATG CAG GAG TCT GTG GCA GGT TCC AAA CTA	617
Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Val Ala Gly Ser Lys Leu	50
GTG CTT CGG TGC GAG ACC AGT TCT GAA TAC TCC TCT CTC AAG TTC AAG	665
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys	65
TGG TTC AAG AAT GGG AGT GAA TTA AGC CGA AAG AAC AAA CCA CAA AAC	713
Trp Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys Pro Gln Asn	85
ATC AAG ATA CAG AAA AGG CCG GGG AAG TCA GAA CTT CGC ATT AGC AAA	761
Ile Lys Ile Gln Lys Arg Pro Gly Lys Ser Glu Leu Arg Ile Ser Lys	100
GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA	809
Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys	115

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FIG. 18B

APPROVED	O.G. FIG.
	CLASS SUBCLASS
BY	DRAFTSMAN

CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC	857
Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn	
120 125 130	
GAG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT	905
Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser	
135 140 145	
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT	953
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr	
150 155 160 165	
TCT TCA TCC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG	1001
Ser Ser Ser Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys	
170 175 180	
TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC	1049
Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe	
185 190 195	
ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC AAG TGC CCA	1097
Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro	
200 205 210	
AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC	1145
Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe	
215 220 225	
TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAGGCGCATG	1191
Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu	
230 235 240	
CTCAGTCGGT GCCGCTTTCT TGTTGCCGCA TCTCCCCTCA GATTCAACCT AGAGCTAGAT	1251
GCGTTTTACC AGGTCTAACA TTGACTGCCT CTGCCTGTCG CATGAGAACA TTAACACAAG	1311
CGATTGTATG ACTTCCTCTG TCCGTGACTA GTGGGCTCTG AGCTACTCGT AGGTGCGTAA	1371
GGCTCCAGTG TTTCTGAAAT TGATCTTGAA TTACTGTGAT ACGACATGAT AGTCCCTCTC	1431
ACCCAGTGCA ATGACAATAA AGGCCTTGAA AAGTCTCACT TTTATTGAGA AAATAAAAAAT	1491
CGTTCCACGG GACAGTCCCT CTTCTTTATA AAATGACCCT ATCCTTGAAA AGGAGGTGTG	1551
TTAAGTTGTA ACCAGTACAC ACTTGAAATG ATGGTAAGTT CGCTTCGGTT CAGAATGTGT	1611
TCTTTCTGAC AAATAAACAG AATAAAAAAA AAAAAAAAAA A	1652